

## RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/789,526A

Source: JFW/LG

Date Processed by STIC: 9/19/06

# *ENTERED*



IFW16

## RAW SEQUENCE LISTING

DATE: 09/19/2006

PATENT APPLICATION: US/10/789,526A

TIME: 13:18:04

Input Set : A:\PTO.SS.txt

Output Set: N:\CRF4\09192006\J789526A.raw

3 <110> APPLICANT: George Tachas  
 4 Kenneth W. Dobie  
 5 Ravi Jain  
 6 Christopher Ian Belyea  
 7 Mark Andrew Heffernan  
 9 <120> TITLE OF INVENTION: MODULATION OF GROWTH HORMONE RECEPTOR EXPRESSION AND  
 10 INSULIN LIKE GROWTH FACTOR EXPRESSION  
 12 <130> FILE REFERENCE: BIOL0002US  
 14 <140> CURRENT APPLICATION NUMBER: 10/789,526A  
 15 <141> CURRENT FILING DATE: 2004-02-26  
 17 <150> PRIOR APPLICATION NUMBER: 60/451,455  
 18 <151> PRIOR FILING DATE: 2003-02-28  
 20 <160> NUMBER OF SEQ ID NOS: 272  
 23 <210> SEQ ID NO: 1  
 24 <211> LENGTH: 20  
 25 <212> TYPE: DNA  
 26 <213> ORGANISM: Artificial Sequence  
 28 <220> FEATURE:  
 30 <223> OTHER INFORMATION: Antisense Oligonucleotide  
 32 <400> SEQUENCE: 1  
 33 tccgtcatcg ctctcaggg 20  
 36 <210> SEQ ID NO: 2  
 37 <211> LENGTH: 20  
 38 <212> TYPE: DNA  
 39 <213> ORGANISM: Artificial Sequence  
 41 <220> FEATURE:  
 43 <223> OTHER INFORMATION: Antisense Oligonucleotide  
 45 <400> SEQUENCE: 2  
 46 gtgcgcgcga gcccgaaatc 20  
 49 <210> SEQ ID NO: 3  
 50 <211> LENGTH: 20  
 51 <212> TYPE: DNA  
 52 <213> ORGANISM: Artificial Sequence  
 54 <220> FEATURE:  
 56 <223> OTHER INFORMATION: Antisense Oligonucleotide  
 58 <400> SEQUENCE: 3  
 59 atgcattctg cccccaagga 20  
 62 <210> SEQ ID NO: 4  
 63 <211> LENGTH: 4414  
 64 <212> TYPE: DNA  
 65 <213> ORGANISM: H. sapiens  
 67 <220> FEATURE:  
 69 <220> FEATURE:

(pg. 6-7)

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71 <222> LOCATION: (44)...(1960)
73 <400> SEQUENCE: 4
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75                                     Met Asp Leu Trp
76                                     1
78 cag ctg ctg ttg acc ttg gca ctg gca gga tca agt gat gct ttt tct      103
79 Gln Leu Leu Leu Thr Leu Ala Leu Ala Gly Ser Ser Asp Ala Phe Ser
80   5          10          15          20
82 gga agt gag gcc aca gca gct atc ctt agc aga gca ccc tgg agt ctg      151
83 Gly Ser Glu Ala Thr Ala Ala Ile Leu Ser Arg Ala Pro Trp Ser Leu
84          25          30          35
86 caa agt gtt aat cca ggc cta aag aca aat tct tct aag gag cct aaa      199
87 Gln Ser Val Asn Pro Gly Leu Lys Thr Asn Ser Ser Lys Glu Pro Lys
88          40          45          50
90 ttc acc aag tgc cgt tca cct gag cga gag act ttt tca tgc cac tgg      247
91 Phe Thr Lys Cys Arg Ser Pro Glu Arg Glu Thr Phe Ser Cys His Trp
92          55          60          65
94 aca gat gag gtt cat cat ggt aca aag aac cta gga ccc ata cag ctg      295
95 Thr Asp Glu Val His His Gly Thr Lys Asn Leu Gly Pro Ile Gln Leu
96          70          75          80
98 ttc tat acc aga agg aac act caa gaa tgg act caa gaa tgg aaa gaa      343
99 Phe Tyr Thr Arg Arg Asn Thr Gln Glu Trp Thr Gln Glu Trp Lys Glu
100  85          90          95          100
102 tgc cct gat tat gtt tct gct ggg gaa aac agc tgt tac ttt aat tca      391
103 Cys Pro Asp Tyr Val Ser Ala Gly Glu Asn Ser Cys Tyr Phe Asn Ser
104          105          110          115
106 tcg ttt acc tcc atc tgg ata cct tat tgt atc aag cta act agc aat      439
107 Ser Phe Thr Ser Ile Trp Ile Pro Tyr Cys Ile Lys Leu Thr Ser Asn
108          120          125          130
110 ggt ggt aca gtg gat gaa aag tgt ttc tct gtt gat gaa ata gtg caa      487
111 Gly Gly Thr Val Asp Glu Lys Cys Phe Ser Val Asp Glu Ile Val Gln
112          135          140          145
114 cca gat cca ccc att gcc ctc aac tgg act tta ctg aac gtc agt tta      535
115 Pro Asp Pro Pro Ile Ala Leu Asn Trp Thr Leu Leu Asn Val Ser Leu
116          150          155          160
118 act ggg att cat gca gat atc caa gtg aga tgg gaa gca cca cgc aat      583
119 Thr Gly Ile His Ala Asp Ile Gln Val Arg Trp Glu Ala Pro Arg Asn
120 165          170          175          180
122 gca gat att cag aaa gga tgg atg gtt ctg gag tat gaa ctt caa tac      631
123 Ala Asp Ile Gln Lys Gly Trp Met Val Leu Glu Tyr Glu Leu Gln Tyr
124          185          190          195
126 aaa gaa gta aat gaa act aaa tgg aaa atg atg gac cct ata ttg aca      679
127 Lys Glu Val Asn Glu Thr Lys Trp Lys Met Met Asp Pro Ile Leu Thr
128          200          205          210
130 aca tca gtt cca gtg tac tca ttg aaa gtg gat aag gaa tat gaa gtg      727
131 Thr Ser Val Pro Val Tyr Ser Leu Lys Val Asp Lys Glu Tyr Glu Val
132          215          220          225
134 cgt gtg aga tcc aaa caa cga aac tct gga aat tat ggc gag ttc agt      775

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135	Arg	Val	Arg	Ser	Lys	Gln	Arg	Asn	Ser	Gly	Asn	Tyr	Gly	Glu	Phe	Ser	
136		230					235					240					
138	gag	gtg	ctc	tat	gta	aca	ctt	cct	cag	atg	agc	caa	ttt	aca	tgt	gaa	823
139	Glu	Val	Leu	Tyr	Val	Thr	Leu	Pro	Gln	Met	Ser	Gln	Phe	Thr	Cys	Glu	
140	245					250					255					260	
142	gaa	gat	ttc	tac	ttt	cca	tgg	ctc	tta	att	att	atc	ttt	gga	ata	ttt	871
143	Glu	Asp	Phe	Tyr	Phe	Pro	Trp	Leu	Leu	Ile	Ile	Ile	Phe	Gly	Ile	Phe	
144					265					270					275		
146	ggg	cta	aca	gtg	atg	cta	ttt	gta	ttc	tta	ttt	tct	aaa	cag	caa	agg	919
147	Gly	Leu	Thr	Val	Met	Leu	Phe	Val	Phe	Leu	Phe	Ser	Lys	Gln	Gln	Arg	
148				280					285					290			
150	att	aaa	atg	ctg	att	ctg	ccc	cca	ggt	cca	ggt	cca	aag	att	aaa	gga	967
151	Ile	Lys	Met	Leu	Ile	Leu	Pro	Pro	Val	Pro	Val	Pro	Lys	Ile	Lys	Gly	
152		295					300						305				
154	atc	gat	cca	gat	ctc	ctc	aag	gaa	gga	aaa	tta	gag	gag	gtg	aac	aca	1015
155	Ile	Asp	Pro	Asp	Leu	Leu	Lys	Glu	Gly	Lys	Leu	Glu	Glu	Val	Asn	Thr	
156		310					315					320					
158	atc	tta	gcc	att	cat	gat	agc	tat	aaa	ccc	gaa	ttc	cac	agt	gat	gac	1063
159	Ile	Leu	Ala	Ile	His	Asp	Ser	Tyr	Lys	Pro	Glu	Phe	His	Ser	Asp	Asp	
160	325					330					335				340		
162	tct	tgg	ggt	gaa	ttt	att	gag	cta	gat	att	gat	gag	cca	gat	gaa	aag	1111
163	Ser	Trp	Val	Glu	Phe	Ile	Glu	Leu	Asp	Ile	Asp	Glu	Pro	Asp	Glu	Lys	
164					345					350					355		
166	act	gag	gaa	tca	gac	aca	gac	aga	ctt	cta	agc	agt	gac	cat	gag	aaa	1159
167	Thr	Glu	Glu	Ser	Asp	Thr	Asp	Arg	Leu	Leu	Ser	Ser	Asp	His	Glu	Lys	
168				360						365				370			
170	tca	cat	agt	aac	cta	ggg	gtg	aag	gat	ggc	gac	tct	gga	cgt	acc	agc	1207
171	Ser	His	Ser	Asn	Leu	Gly	Val	Lys	Asp	Gly	Asp	Ser	Gly	Arg	Thr	Ser	
172		375						380					385				
174	tgt	tgt	gaa	cct	gac	att	ctg	gag	act	gat	ttc	aat	gcc	aat	gac	ata	1255
175	Cys	Cys	Glu	Pro	Asp	Ile	Leu	Glu	Thr	Asp	Phe	Asn	Ala	Asn	Asp	Ile	
176		390					395					400					
178	cat	gag	ggt	acc	tca	gag	ggt	gct	cag	cca	cag	agg	tta	aaa	ggg	gaa	1303
179	His	Glu	Gly	Thr	Ser	Glu	Val	Ala	Gln	Pro	Gln	Arg	Leu	Lys	Gly	Glu	
180	405					410					415				420		
182	gca	gat	ctc	tta	tgc	ctt	gac	cag	aag	aat	caa	aat	aac	tca	cct	tat	1351
183	Ala	Asp	Leu	Leu	Cys	Leu	Asp	Gln	Lys	Asn	Gln	Asn	Asn	Ser	Pro	Tyr	
184				425						430				435			
186	cat	gat	gct	tgc	cct	gct	act	cag	cag	ccc	agt	ggt	atc	caa	gca	gag	1399
187	His	Asp	Ala	Cys	Pro	Ala	Thr	Gln	Gln	Pro	Ser	Val	Ile	Gln	Ala	Glu	
188				440					445				450				
190	aaa	aac	aaa	cca	caa	cca	ctt	cct	act	gaa	gga	gct	gag	tca	act	cac	1447
191	Lys	Asn	Lys	Pro	Gln	Pro	Leu	Pro	Thr	Glu	Gly	Ala	Glu	Ser	Thr	His	
192		455						460					465				
194	caa	gct	gcc	cat	att	cag	cta	agc	aat	cca	agt	tca	ctg	tca	aac	atc	1495
195	Gln	Ala	Ala	His	Ile	Gln	Leu	Ser	Asn	Pro	Ser	Ser	Leu	Ser	Asn	Ile	
196		470					475					480					
198	gac	ttt	tat	gcc	cag	gtg	agc	gac	att	aca	cca	gca	ggt	agt	gtg	gtc	1543
199	Asp	Phe	Tyr	Ala	Gln	Val	Ser	Asp	Ile	Thr	Pro	Ala	Gly	Ser	Val	Val	

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202	ctt	tcc	ccg	ggc	caa	aag	aat	aag	gca	ggg	atg	tcc	caa	tgt	gac	atg	1591
203	Leu	Ser	Pro	Gly	Gln	Lys	Asn	Lys	Ala	Gly	Met	Ser	Gln	Cys	Asp	Met	
204					505					510					515		
206	cac	ccg	gaa	atg	gtc	tca	ctc	tgc	caa	gaa	aac	ttc	ctt	atg	gac	aat	1639
207	His	Pro	Glu	Met	Val	Ser	Leu	Cys	Gln	Glu	Asn	Phe	Leu	Met	Asp	Asn	
208					520					525					530		
210	gcc	tac	ttc	tgt	gag	gca	gat	gcc	aaa	aag	tgc	atc	cct	gtg	gct	cct	1687
211	Ala	Tyr	Phe	Cys	Glu	Ala	Asp	Ala	Lys	Lys	Cys	Ile	Pro	Val	Ala	Pro	
212					535					540					545		
214	cac	atc	aag	gtt	gaa	tca	cac	ata	cag	cca	agc	tta	aac	caa	gag	gac	1735
215	His	Ile	Lys	Val	Glu	Ser	His	Ile	Gln	Pro	Ser	Leu	Asn	Gln	Glu	Asp	
216					550					555					560		
218	att	tac	atc	acc	aca	gaa	agc	ctt	acc	act	gct	gct	ggg	agg	cct	ggg	1783
219	Ile	Tyr	Ile	Thr	Thr	Glu	Ser	Leu	Thr	Thr	Ala	Ala	Gly	Arg	Pro	Gly	
220	565					570					575					580	
222	aca	gga	gaa	cat	gtt	cca	ggt	tct	gag	atg	cct	gtc	cca	gac	tat	acc	1831
223	Thr	Gly	Glu	His	Val	Pro	Gly	Ser	Glu	Met	Pro	Val	Pro	Asp	Tyr	Thr	
224					585					590					595		
226	tcc	att	cat	ata	gta	cag	tcc	cca	cag	ggc	ctc	ata	ctc	aat	gcg	act	1879
227	Ser	Ile	His	Ile	Val	Gln	Ser	Pro	Gln	Gly	Leu	Ile	Leu	Asn	Ala	Thr	
228					600					605					610		
230	gcc	ttg	ccc	ttg	cct	gac	aaa	gag	ttt	ctc	tca	tca	tgt	ggc	tat	gtg	1927
231	Ala	Leu	Pro	Leu	Pro	Asp	Lys	Glu	Phe	Leu	Ser	Ser	Cys	Gly	Tyr	Val	
232					615					620					625		
234	agc	aca	gac	caa	ctg	aac	aaa	atc	atg	cct	tag	cctttctttg	gtttcccaag				1980
235	Ser	Thr	Asp	Gln	Leu	Asn	Lys	Ile	Met	Pro							
236					630					635							
238	agctacgtat	ttaatagcaa	agaattgact	ggggcaataa	cgtttaagcc	aaaacaatgt											2040
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244	tgtgcaatgt	aaatatttta	aagaattgtg	tcagactggt	tagtagcagt	gattgtctta											2220
246	atattgtggg	tgtaattttt	tgatactaag	cattgaatgg	ctatgtttttt	aatgtatagt											2280
248	aatcacgct	ttttgaaaaa	gcgaaaaaat	caggtggctt	ttgcggttca	ggaaaattga											2340
250	atgcaaacca	tagcacaggc	taattttttt	ttgtttctta	aataagaaac	ttttttattt											2400
252	aaaaaactaa	aaactagagg	tgagaaatth	aaactataag	caagaaggca	aaaatagttt											2460
254	ggatatgtaa	aacattttact	ttgacataaa	gttgataaag	attttttaat	aatttagact											2520
256	tcaagcatgg	ctattttata	ttacactaca	cactgtgtac	tgacgttggt	atgacccttc											2580
258	taaggagtgt	agcaactaca	gtctaaagct	ggtttaatgt	tttggccaat	gcacctaaag											2640
260	aaaaacaaac	tcgtttttta	caaagccctt	ttatacctcc	ccagactcct	tcaacaattc											2700
262	taaaatgatt	gtagtaattct	gcattatttg	aatataattg	ttttatctga	attttttaac											2760
264	aagtattttgt	taatttagaa	aacttttaaag	cgtttgcaca	gatcaactta	ccaggcacca											2820
266	aaagaagtaa	aagcaaaaaa	gaaaaccttt	cttcaccaa	tcttggttga	tgccaaaaaa											2880
268	aaatacatgc	taagagaagt	agaaatcata	gctgggttcac	actgaccaag	atacttaagt											2940
270	gctgcaattg	cacgcggagt	gagtttttta	gtgcgtgcag	atggtgagag	ataagatcta											3000
272	tagcctctgc	agcggaatct	gttcacaccc	aacttggttt	tgctacataa	ttatccagga											3060
274	aggggaataag	gtacaagaag	cattttgtta	gttgaagcaa	atcgaatgaa	attaactggg											3120
276	taatgaaaca	aagagttcaa	gaaataagtt	tttgtttcac	agcctataac	cagacacata											3180
278	ctcattttttc	atgataatga	acagaacata	gacagaagaa	acaaggtttt	cagtccccac											3240

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282 aggattttatt taaaatagca aaagaagaag tttcatcatt ttttacttcc tctctgagtg 3360
284 gactggcctc aaagcaagca ttcagaagaa aaagaagcaa cctcagtaat ttagaaatca 3420
286 ttttgcaatc ccttaatatc ctaaacaatca ttcatttttg ttggtgtgtg ttggtgtgag 3480
288 acagagtctc gctctgtcgc caggctagag tgcggtggcg cgatcttgac tcaactgcaat 3540
290 ctccacctcc cacaggttca ggcgattccc gtgcctcagc ctcttgagta gctgggacta 3600
292 caggcacgca ccacctgccc aggctaattt ttttgtattt tagcagagac ggggtttcac 3660
294 catgttgccc aggatggtct cgagtctcct gacctcgtga tccacctgac tcggcctccc 3720
296 aaagtgtctg gattacaggt gtaagccacc gtgcccagcc ctaaacaatca ttcttgagag 3780
298 cattgggata tctcctgaaa aggtttatga aaaagaagaa tctcatctca gtgaagaata 3840
300 cttctcattt tttaaaaaag cttaaaactt tgaagttagc ttttaactta atagtatttc 3900
302 ccattttatcg cagacctttt ttaggaagca agcttaatgg ctgataattt taaattctct 3960
304 ctcttgcaag aaggactatg aaaagctaga attgagtggt taaagttcaa catgttattt 4020
306 gtaatagatg tttgatagat tttctgctac tttgctgcta tggttttctc caagagctac 4080
308 ataatttagt ttcataataa gtatcatcag tgtagaacct aattcaattc aaagctgtgt 4140
310 gtttggaaga ctatcttact atttcacaac agcctgacaa catttctata gccaaaaata 4200
312 gctaaatacc tcaatcagtc tcagaatgtc attttggtac tttggtggcc acataagcca 4260
314 ttattcacta gtatgactag ttgtgtctgg cagtttatat ttaactctct ttatgtctgt 4320
316 ggattttttc cttcaaagtt taataaattt attttcttgg attcctgata atgtgcttct 4380
318 gttatcaaac accaacataa aaatgatcta aacc 4414

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321 &lt;210&gt; SEQ ID NO: 5

322 &lt;211&gt; LENGTH: 21

323 &lt;212&gt; TYPE: DNA

324 &lt;213&gt; ORGANISM: Artificial Sequence

326 &lt;220&gt; FEATURE:

328 &lt;223&gt; OTHER INFORMATION: PCR Primer

330 &lt;400&gt; SEQUENCE: 5

331 gatgtcccaa tgtgacatgc a 21

334 &lt;210&gt; SEQ ID NO: 6

335 &lt;211&gt; LENGTH: 26

336 &lt;212&gt; TYPE: DNA

337 &lt;213&gt; ORGANISM: Artificial Sequence

339 &lt;220&gt; FEATURE:

341 &lt;223&gt; OTHER INFORMATION: PCR Primer

343 &lt;400&gt; SEQUENCE: 6

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348 &lt;211&gt; LENGTH: 26

349 &lt;212&gt; TYPE: DNA

350 &lt;213&gt; ORGANISM: Artificial Sequence

352 &lt;220&gt; FEATURE:

354 &lt;223&gt; OTHER INFORMATION: PCR Probe

356 &lt;400&gt; SEQUENCE: 7

357 ccggaaatgg tctcactctg ccaaga 26

360 &lt;210&gt; SEQ ID NO: 8

361 &lt;211&gt; LENGTH: 19

362 &lt;212&gt; TYPE: DNA

363 &lt;213&gt; ORGANISM: Artificial Sequence

365 &lt;220&gt; FEATURE:

RAW SEQUENCE LISTING ERROR SUMMARY  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:11; N Pos. 2636,2666,2759,2789,3326,3352,3503,3666,3668  
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Seq#:100; N Pos. 9593,9594,9595,9596,9597,9598,9599,9600,9601,9602,9603  
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Seq#:100; N Pos. 14497,14498,14499,14500,14501,14502,14503,14504,14505  
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RAW SEQUENCE LISTING ERROR SUMMARY      DATE: 09/19/2006  
PATENT APPLICATION: US/10/789,526A      TIME: 13:18:05

Input Set : A:\PTO.SS.txt  
Output Set: N:\CRF4\09192006\J789526A.raw

Seq#:100; N Pos. 20196,20197,25938,25939,25940,25941,25942,25943,25944  
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Seq#:100; N Pos. 25972,25973,25974,25975,25976,25977,25978,25979,25980  
Seq#:100; N Pos. 25981,25982,25983,25984,25985,25986,25987,25988,25989  
Seq#:100; N Pos. 25990,25991,25992,25993,25994,25995,25996,25997,25998

**VERIFICATION SUMMARY**

DATE: 09/19/2006

PATENT APPLICATION: US/10/789,526A

TIME: 13:18:05

Input Set : A:\PTO.SS.txt

Output Set: N:\CRF4\09192006\J789526A.raw

L:654 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:2632  
M:341 Repeated in SeqNo=11  
L:3137 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:98 after pos.:2400  
M:341 Repeated in SeqNo=98  
L:3336 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:99 after pos.:2460  
M:341 Repeated in SeqNo=99  
L:3426 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:100 after pos.:0  
M:341 Repeated in SeqNo=100